

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 28, 2005, 18:44:48 ; Search time 191 Seconds
(without alignments)
30.124 Million cell updates/sec

Title: US-09-991-627-2
Perfect score: 50
Sequence: 1 NLEKETEGLR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Uniprot_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	191	2 Q8H295	Q8h295 pongo pygma
2	50	100.0	191	2 Q8H296	Q8h296 gorilla gor
3	50	100.0	191	2 Q8H297	Q8h297 pan troglod
4	50	100.0	249	2 Q6LDN9	Q6ldn9 homo sapien
5	50	100.0	249	2 AA51747	AA51747 homo sapi
6	50	100.0	266	1 APAL_RABIT	P09809 corynebacte
7	50	100.0	267	1 APAL_HUMAN	P02647 homo sapien
8	50	100.0	267	1 APAL_MACFA	P15568 macaca fasc
9	50	100.0	267	2 AAQ91811	AAQ91811 homo sapi
10	50	100.0	267	2 AAS68227	AAS68227 homo sapi
11	47	94.0	241	2 Q9TS49	Q9ts49 erinaceus e
12	44	88.0	265	1 APAL_PIG	P18648 sus scrofa
13	42	84.0	264	2 Q9Z2L4	Q9z2l4 mesocricetu
14	41	82.0	191	2 Q8H294	Q8h294 saguinus oe
15	41	82.0	266	1 APAL_CANFA	P02648 canis famil
16	39	78.0	96	2 Q6NN75	Q6nn75 drosophila
17	39	78.0	96	2 AAR96210	AAR96210 drosophil
18	39	78.0	188	1 TPTL_PIG	Q97557 sus scrofa
19	39	78.0	199	1 UBC4_DROME	P52486 drosophila
20	39	78.0	199	2 P91633	P91633 drosophila
21	39	78.0	259	1 APAL_RAT	P04639 rattus norv
22	39	78.0	390	1 TPTL_BOVIN	P27628 bos taurus
23	39	78.0	714	2 Q8PS05	Q8ps05 methanosarc
24	38	76.0	56	2 O02762	O02762 ovis aries
25	38	76.0	142	2 Q85316	Q85316 rabbit fibr
26	38	76.0	190	2 Q9Q8N0	Q9q8n0 myxoma viru
27	38	76.0	190	2 Q9Q902	Q9q902 rabbit fibr
28	38	76.0	265	1 APAL_BOVIN	P15497 bos taurus
29	38	76.0	522	2 Q9N3E3	Q9n3e3 caenorhabdi
30	38	76.0	1734	2 Q7RBR3	Q7rb3 plasmodium
31	38	76.0	1850	2 Q7R220	Q7r220 giardia lam

32	37	74.0	197	2 Q99LE1	Q99le1 mus musculu
33	37	74.0	978	1 RA50_AQUAE	Ra50 aquifex aeo
34	36	72.0	79	2 Q6LD50	Q6ld50 mus sp. apo
35	36	72.0	79	2 AAB35539	Aab35539 mus sp. a
36	36	72.0	139	2 Q9FXP3	Q9fxp3 zinnia eleg
37	36	72.0	170	2 Q9FXP2	Q9fxp2 zinnia eleg
38	36	72.0	211	2 Q7VKD0	Q7vk0 haemophilus
39	36	72.0	227	2 Q9SQK9	Q9sqk9 lycopersico
40	36	72.0	255	2 Q8LFD3	Q8lfd3 arabidopsis
41	36	72.0	263	2 Q08855	Q08855 mus musculu
42	36	72.0	263	2 Q09042	Q09042 mus musculu
43	36	72.0	264	1 APAL_MOUSE	APal mouse
44	36	72.0	284	2 Q8BPD5	Q8bpd5 mus musculu
45	36	72.0	265	1 APAL_TUPGB	APal tupai glis
46	36	72.0	274	2 Q8C089	Q8c089 mus musculu
47	36	72.0	282	2 Q9ZVG2	Q9zvg2 arabidopsis
48	36	72.0	288	2 Q8LC03	Q8lc03 arabidopsis
49	36	72.0	294	2 Q9S7A4	Q9s7a4 arabidopsis
50	36	72.0	301	2 Q43426	Q43426 daucus caro
51	36	72.0	304	2 Q6L4K0	Q6l4k0 solanum dem
52	36	72.0	304	2 AAT40488	Aat40488 solanum d
53	36	72.0	306	2 Q6L467	Q6l467 solanum dem
54	36	72.0	306	2 AAT40518	Aat40518 solanum d
55	36	72.0	308	2 Q43428	Q43428 daucus caro
56	36	72.0	313	2 Q6L452	Q6l452 solanum dem
57	36	72.0	313	2 AAT39931	Aat39931 solanum d
58	36	72.0	330	1 EXL2_MOUSE	EXL2 mouse
59	36	72.0	330	2 Q8C197	Q8c197 mus musculu
60	36	72.0	348	2 Q98KF5	Q98kf5 rhizobium l
61	36	72.0	352	2 Q6F783	Q6f783 acinetobact
62	36	72.0	411	2 Q73R75	Q73r75 treponema d
63	36	72.0	411	2 AAS10713	Aas10713 treponema
64	36	72.0	463	2 Q6NIN9	Q6nin9 corynebacte
65	36	72.0	463	2 CAE49251	Ca49251 corynebac
66	36	72.0	1335	2 Q7VJN2	Q7vln2 prochloroco
67	35	70.0	117	1 GVPK_HALME	Gvpk halobacteri
68	35	70.0	137	2 Q27852	Q27852 methanobact
69	35	70.0	180	2 Q9ETC6	Q9etc6 anabaena ci
70	35	70.0	180	2 Q9F970	Q9f970 anabaena sp
71	35	70.0	180	2 Q9F971	Q9f971 anabaena sp
72	35	70.0	180	2 Q9F972	Q9f972 aphanizomen
73	35	70.0	180	2 Q9F973	Q9f973 anabaena ap
74	35	70.0	180	2 Q9F974	Q9f974 anabaena fl
75	35	70.0	180	2 Q9F976	Q9f976 anabaena sp
76	35	70.0	180	2 Q9F977	Q9f977 anabaena so
77	35	70.0	180	2 Q9F978	Q9f978 anabaena ci
78	35	70.0	188	2 Q8WV38	Q8wv38 homo sapien
79	35	70.0	201	2 Q84Y37	Q84y37 thalicttrum
80	35	70.0	203	2 Q9RG17	Q9rg17 anabaenopsi
81	35	70.0	203	2 Q9RG18	Q9rg18 anabaena ci
82	35	70.0	211	2 Q969X0	Q969x0 homo sapien
83	35	70.0	227	2 Q6TBM0	Q6tbm0 nodularia s
84	35	70.0	227	2 Q6TBM1	Q6tbm1 nodularia s
85	35	70.0	227	2 Q6TBM2	Q6tbm2 nostoc sp.
86	35	70.0	227	2 AAR92056	Aar92056 nostoc sp
87	35	70.0	227	2 AAR92057	Aar92057 nodularia
88	35	70.0	227	2 AAR92058	Aar92058 nodularia
89	35	70.0	234	1 NK4_HUMAN	Nk4001 homo sapien
90	35	70.0	234	2 Q96GK9	Q96gk9 homo sapien
91	35	70.0	273	2 Q7X4A0	Q7x4a0 colyptothrix
92	35	70.0	295	2 Q7X495	Q7x495 chlorogloeo
93	35	70.0	295	2 Q7X496	Q7x496 fischerella
94	35	70.0	295	2 Q7X498	Q7x498 nostoc ento
95	35	70.0	295	2 Q7X4A1	Q7x4a1 anabaena pl
96	35	70.0	295	2 Q8L134	Q8l134 nodularia s
97	35	70.0	295	2 Q8L135	Q8l135 fischerella
98	35	70.0	295	2 Q8L138	Q8l138 chlorogloeo
99	35	70.0	295	2 Q8L143	Q8l143 anabaenopsi
100	35	70.0	295	2 Q8L144	Q8l144 anabaena va
101	35	70.0	295	2 Q8L146	Q8l146 anabaena cy
102	35	70.0	295	2 Q8L147	Q8l147 nostoc linc
103	35	70.0	295	2 Q8L148	Q8l148 calochrix b
104	35	70.0	295	2 Q8L150	Q8l150 anabaena va

105	35	70.0	300	2	Q6NU65	Q6nu65 xenopus lae	178	34	68.0	589	2	Q6INL2	Q6inl2 xenopus lae
106	35	70.0	300	2	AAH68735	Aah68735 xenopus 1	179	34	68.0	589	2	AAH72268	Aah72268 xenopus 1
107	35	70.0	318	2	Q8L998	Q8l998 arabisopsis	180	34	68.0	594	2	Q834d4	Q834d4 enterococcu
108	35	70.0	318	2	Q9LXR8	Q9lxr8 arabisopsis	181	34	68.0	599	2	Q95SH3	Q95sh3 drosophila
109	35	70.0	334	2	Q8ERN3	Q8ern3 oceanobacil	182	34	68.0	621	2	Q7Q003	Q7q003 giardia lam
110	35	70.0	338	2	Q8RD46	Q8rd46 thermoanaer	183	34	68.0	634	2	Q8CJ83	Q8cj83 rattus norv
111	35	70.0	332	2	Q7WVB7	Q7wvb7 staphylococ	184	34	68.0	637	2	Q8N825	Q8n825 homo sapien
112	35	70.0	448	2	Q21178	Q21178 caenorhabdi	185	34	68.0	651	2	Q8NCU84	Q8ncj84 rattus norv
113	35	70.0	462	2	Q7U8T1	Q7u8t1 synchococc	186	34	68.0	671	2	Q8CJ98	Q8cj98 rattus norv
114	35	70.0	486	2	Q8Q0A3	Q8q0a3 methanosaer	187	34	68.0	678	2	Q8BRJ9	Q8brj9 mus musculu
115	35	70.0	499	2	Q6ZSE3	Q6zes3 synchocyst	188	34	68.0	688	2	Q8CJ99	Q8cj99 rattus norv
116	35	70.0	499	2	BAD02017	Bad02017 synchocyst	189	34	68.0	728	2	Q8QZ68	Q8qz68 tomato mild
117	35	70.0	621	1	RPOC NOSCO	Fl4563 nostoc comm	190	34	68.0	752	2	Q7VD86	Q7vd86 prochloroco
118	35	70.0	625	1	RPOC ANASP	P22704 anabaena sp	191	34	68.0	787	2	Q7Q0Y9	Q7qy9 giardia lam
119	35	70.0	657	2	Q83140	Q83140 treponema p	192	34	68.0	810	2	Q9UIA9	Q9uia9 leishmania
120	35	70.0	710	2	Q6IP90	Q6ip90 xenopus lae	193	34	68.0	924	2	Q6H4Y5	Q6h4y5 oryza sativ
121	35	70.0	710	2	AAH72027	Aah72027 xenopus 1	194	34	68.0	959	2	Q8BY82	Q8by82 mus musculu
122	35	70.0	862	2	Q6ZSE3	Q6zes3 homo sapien	195	34	68.0	983	1	4ET_MOUSE	Q9est3 mus musculu
123	35	70.0	862	2	BAC87010	Bac87010 homo sapi	196	34	68.0	983	2	Q8CFW0	Q8cfw0 mus musculu
124	35	70.0	988	2	Q6SLB1	Q6slb1 gibberella	197	34	68.0	985	1	4ET_HUMAN	Q9nra8 homo sapien
125	35	70.0	988	2	AAH72027	Aar30127 gibberell	198	34	68.0	985	2	CAG30272	Cag30272 homo sapi
126	35	70.0	1092	2	Q7RR39	Q7rr39 plasmodium	199	34	68.0	1014	2	Q35082	Q35082 mus musculu
127	35	70.0	1112	2	Q7US98	Q7us98 rhodopirell	200	34	68.0	1014	2	Q70175	Q70175 mus musculu
128	35	70.0	1223	2	Q6FUN1	Q6fun1 candida gla	201	34	68.0	1014	2	Q922Y9	Q922y9 rattus norv
129	35	70.0	1310	2	Q949K0	Q949k0 lycopersico	202	34	68.0	1037	2	Q7Q5D0	Q7q5d0 anopheles g
130	35	70.0	1748	2	Q57613	Q57613 gallus gall	203	34	68.0	1112	2	Q8JTI3	Q8jti3 little cher
131	35	70.0	1780	2	Q6TV07	Q6tv07 homo sapien	204	34	68.0	1178	2	Q84F12	Q84f12 cytophaga h
132	35	70.0	1780	2	AAH72027	Aar25619 homo sapi	205	34	68.0	1195	1	YK76 YEAST	P36168 saccharomyc
133	35	70.0	1840	2	Q90831	Q90831 gallus gall	206	34	68.0	1226	2	Q84VE4	Q84ve4 oryza sativ
134	35	70.0	2617	2	Q7ROQ0	Q7roq0 giardia lam	207	34	68.0	1248	2	Q7XPJ0	Q7xpi0 oryza sativ
135	34	68.0	55	2	Q6FP9K2	Q6fp9k2 acinetobact	208	34	68.0	1290	1	SMC4_XENLA	P50532 xenopus lae
136	34	68.0	114	1	Y467_BUCAI	P57539 buchnera ap	209	34	68.0	1467	2	Q8CHH8	Q8chh8 mus musculu
137	34	68.0	116	2	Q6JSY6	Q6jsy6 australobiu	210	34	68.0	1528	2	Q991N1	Q991n1 little cher
138	34	68.0	116	2	AAQ77086	Aaq77086 australob	211	34	68.0	1588	2	Q9BSK9	Q9bsk9 mus musculu
139	34	68.0	142	2	Q61384	Q61384 mus musculu	212	34	68.0	1593	2	Q92601	Q92601 homo sapien
140	34	68.0	155	2	Q6CGB4	Q6cgb4 yarrowia li	213	34	68.0	1594	2	Q8TDY2	Q8tdy2 homo sapien
141	34	68.0	182	2	Q9C4R0	Q9c4r0 methanococc	214	34	68.0	1594	2	Q8WVU9	Q8wvu9 homo sapien
142	34	68.0	186	2	Q6LWP0	Q6lwp0 methanococc	215	34	68.0	1627	2	Q7R264	Q7r264 giardia lam
143	34	68.0	186	2	CAF31225	CAF31225 methanococ	216	34	68.0	1627	2	Q962Q0	Q962q0 giardia lam
144	34	68.0	188	1	FLAC METVO	O06636 methanococc	217	34	68.0	1640	2	Q7T738	Q7t738 little cher
145	34	68.0	198	2	Q8BZL5	Q8bz15 mus musculu	218	34	68.0	1680	2	Q991N2	Q991n2 little cher
146	34	68.0	205	2	Q6BVM3	Q6bvm3 debaryomyce	219	34	68.0	1984	2	Q9VZ85	Q9vz85 drosophila
147	34	68.0	205	2	Q8DVM4	Q8dvm4 streptococc	220	34	68.0	1984	2	Q8WQ0M	Q8wqm0 drosophila
148	34	68.0	222	1	BID2_YERPE	Q9ag4 streptococc	221	34	68.0	2033	1	EVPL_HUMAN	Q9wml0 homo sapien
149	34	68.0	222	2	Q93AN8	Q93an8 yersinia ps	222	34	68.0	2183	2	Q98589	Q98589 subacute sc
150	34	68.0	245	2	Q8ZX05	Q8zx05 pyrobaculum	223	34	68.0	2183	2	O45614	O45614 caenorhabdi
151	34	68.0	254	1	MOAC_AQUAE	Q66810 aquifex ao	224	33	67.0	3102	2	O45614	Q73n94 treponema d
152	34	68.0	271	2	P89104	P89104 saccharomyc	225	33	67.0	522	2	Q73N94	Q73n94 treponema d
153	34	68.0	291	2	Q93VD1	Q93vdi oryza sativ	226	33	66.0	522	2	Q8HR55	Q8hr55 clivia gard
154	34	68.0	310	2	Q95Y78	Q95y78 caenorhabdi	227	33	66.0	74	2	Q72TG2	Q72tg2 leptospira
155	34	68.0	328	2	Q6GPR0	Q6gpr0 xenopus lae	228	33	66.0	90	2	Q8FIW2	Q8fiw2 leptospira
156	34	68.0	333	2	Q9BU49	Q9bu49 homo sapien	229	33	66.0	90	2	AA569666	AA569666 leptospir
157	34	68.0	333	2	Q96D63	Q96d63 homo sapien	230	33	66.0	92	2	Q6T6S6	Q6t6s6 bitis gabon
158	34	68.0	361	2	Q6BQ02	Q6bq02 debaryomyce	231	33	66.0	92	2	AA255557	AA255557 bitis gab
159	34	68.0	375	2	Q947A1	Q947a1 prionitis 1	232	33	66.0	107	2	Q8T557	Q8t557 debaryomyce
160	34	68.0	378	2	Q8HYU6	Q8hyu6 oryctolagus	233	33	66.0	107	2	Q8BKC3	Q8bkc3 drosophila
161	34	68.0	422	1	K1CW_HUMAN	Q9c075 homo sapien	234	33	66.0	113	2	Q6BKC3	Q6bkc3 drosophila
162	34	68.0	422	1	K1CW_MOUSE	Q9c075 homo sapien	235	33	66.0	156	2	Q9AJN8	Q9ajn8 caulobacter
163	34	68.0	422	2	Q8TC04	Q8tc04 homo sapien	236	33	66.0	161	2	Q8RC07	Q8rc07 thermoanaer
164	34	68.0	422	2	Q6IFW4	Q6ifw4 rattus norv	237	33	66.0	180	2	Q9F375	Q9f375 anabaena pe
165	34	68.0	422	2	Q8CB30	Q8cb30 mus musculu	238	33	66.0	183	1	TR13_HUMAN	Q15645 homo sapien
166	34	68.0	422	2	BAC29649	Bac29649 mus muscu	239	33	66.0	184	2	Q6DT75	Q6dt75 arabisopsis
167	34	68.0	436	2	Q6PJR2	Q6pjr2 homo sapien	240	33	66.0	203	1	RPOC_F1SMU	R42074 fischerella
168	34	68.0	436	2	AAH12734	Aah12734 homo sapi	241	33	66.0	203	2	Q46580	Q46580 dermocarpa
169	34	68.0	466	2	Q6WIE1	Q6wie1 bacterioph	242	33	66.0	203	2	Q8RG20	Q8rg20 cylindrospe
170	34	68.0	466	2	AAQ64081	Aaq64081 bacteriop	243	33	66.0	211	2	Q8H7A8	Q8h7a8 arabisopsis
171	34	68.0	497	2	Q8ZRZ7	Q8zrz7 salmonella	244	33	66.0	213	2	Q9ZDE0	Q9zde0 rickettsia
172	34	68.0	509	2	Q8FLC3	Q8flc3 escherichia	245	33	66.0	226	2	Q7P7J6	Q7p7j6 fusobacteri
173	34	68.0	512	2	Q944K1	Q944k1 arabisopsis	246	33	66.0	226	2	Q8RFI0	Q8rfi0 fusobacteri
174	34	68.0	514	2	Q8RWT8	Q8rwt8 arabisopsis	247	33	66.0	227	2	Q6TBL9	Q6tbl9 microcystis
175	34	68.0	532	2	Q7V3T9	Q7v3t9 prochloroco	248	33	66.0	227	2	Q6TBM3	Q6tbm3 anabaena ci
176	34	68.0	550	2	Q70621	Q70621 mus musculu	249	33	66.0	227	2	Q6TBM4	Q6tbm4 anabaena sp
177	34	68.0	573	2	O65395	O65395 arabisopsis	250	33	66.0	227	2	AA92054	AA92054 anabaena

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OM protein - protein search, using sw model

Run on: January 28, 2005, 18:43:43 ; Search time 154 Seconds

(without alignments)
23.294 Million cell updates/sec

Title: US-09-991-627-2

Perfect score: 50

Sequence: 1 NLEKETEGLR 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	10	7	ADD94064 Human apo
2	50	100.0	16	4	AAG62607 Apolipop
3	50	100.0	119	4	AAU30468 Novel hum
4	50	100.0	120	4	AAU30469 Novel hum
5	50	100.0	120	4	AAU30267 Novel hum
6	50	100.0	160	6	ABP5964 Human GEN
7	50	100.0	166	4	AAU28372 Novel hum
8	50	100.0	168	5	AAE24649 Human MSP
9	50	100.0	168	5	AAE24648 Human MSP
10	50	100.0	170	6	ADA61215 Human 18K
11	50	100.0	201	5	AAE24644 Human non
12	50	100.0	201	5	AAE24650 Human MSP
13	50	100.0	201	5	AAE24651 Human MSP
14	50	100.0	207	5	ABP53596 Human NOV
15	50	100.0	211	5	ABG69598 Human NOV
16	50	100.0	211	7	ADJ83023 Human NOV
17	50	100.0	212	5	AAE24643 Human his
18	50	100.0	221	4	AAU29835 Novel hum
19	50	100.0	240	5	ABP53595 Human NOV
20	50	100.0	240	5	ABG69597 Human NOV
21	50	100.0	240	1	ADJ83021 Human NOV
22	50	100.0	243	1	AAU1082 Sequence
23	50	100.0	243	5	AAE24653 Human apo
24	50	100.0	243	5	ABG97579 Human apo
25	50	100.0	243	7	ADD29960 Mutant ma

26	50	100.0	243	8	AD006580
27	50	100.0	244	4	AAU28184
28	50	100.0	244	5	ABG97580
29	50	100.0	249	7	ADJ83085
30	50	100.0	250	5	AAE24642
31	50	100.0	252	6	ABR43302
32	50	100.0	254	7	ADD29962
33	50	100.0	254	7	ADD29961
34	50	100.0	258	5	ABG97582
35	50	100.0	261	5	ABG97598
36	50	100.0	264	2	AAE24644
37	50	100.0	264	2	AAE24647
38	50	100.0	267	1	AAE24647
39	50	100.0	267	1	AAE24647
40	50	100.0	267	2	AAE24647
41	50	100.0	267	2	AAE24647
42	50	100.0	267	2	AAE24647
43	50	100.0	267	2	AAE24647
44	50	100.0	267	4	AAE24647
45	50	100.0	267	5	AAE24647
46	50	100.0	267	5	AAE24647
47	50	100.0	267	6	AAE24647
48	50	100.0	267	6	AAE24647
49	50	100.0	267	6	AAE24647
50	50	100.0	267	6	AAE24647
51	50	100.0	267	7	AAE24647
52	50	100.0	267	7	AAE24647
53	50	100.0	267	7	AAE24647
54	50	100.0	267	7	AAE24647
55	50	100.0	267	7	AAE24647
56	50	100.0	267	8	AAE24647
57	50	100.0	267	8	AAE24647
58	50	100.0	268	1	AAE24647
59	50	100.0	273	5	AAE24647
60	50	100.0	275	6	AAE24647
61	50	100.0	299	4	AAU33170
62	50	100.0	301	5	ABG97583
63	50	100.0	301	5	ABG97581
64	50	100.0	304	5	ABG97584
65	50	100.0	304	5	ABG97586
66	50	100.0	304	5	ABG97585
67	50	100.0	306	5	ABG97588
68	50	100.0	306	5	ABG97587
69	50	100.0	306	5	ABG97589
70	50	100.0	316	5	ABG97599
71	50	100.0	316	5	ABG97596
72	50	100.0	323	5	ABG97602
73	50	100.0	323	5	ABG97601
74	50	100.0	323	5	ABG97600
75	50	100.0	325	5	ABG97603
76	50	100.0	325	5	ABG97604
77	50	100.0	325	5	ABG97605
78	50	100.0	329	5	ABG97592
79	50	100.0	336	5	ABG97594
80	50	100.0	337	5	ABG97595
81	50	100.0	344	5	ABG97606
82	50	100.0	392	5	AAE24652
83	50	100.0	414	5	AAE24646
84	50	100.0	422	5	AAE24647
85	47	94.0	151	4	AAU02278
86	47	94.0	180	8	AAU02278
87	46	92.0	318	4	AAU02268
88	42	84.0	154	4	AAU02095
89	39	78.0	199	4	ABG63741
90	39	78.0	259	7	ADP30722
91	39	78.0	259	7	ADP30714
92	39	78.0	259	7	ADP30724
93	39	78.0	259	7	ADP30726
94	36	72.0	201	3	AAU21619
95	36	72.0	212	3	AAU21618
96	36	72.0	255	3	AAU21617
97	36	72.0	280	3	AAU08396
98	36	72.0	288	3	AAU08395

Ado06580	Apolipop
Aau28184	Novel hum
Abg97580	Human apo
Adj83085	Human pro
Aae24642	Human pro
Abr43302	Human lip
Add29962	Mature hu
Add29961	Mutant ma
Abg97582	Human apo
Abg97598	Human apo
Aar56864	Apo-lipop
Aar56863	Apo-lipop
Aap61079	Assumed h
Aap82128	Entire hu
Aar72705	Human apo
Aar34032	Sequence
Aaw08602	Human apo
Aay18675	Human apo
Aab47620	Full leng
Aao15892	Human apo
Abg97593	Human apo
Abr44031	Human mut
Abr44032	Human mut
Abp57065	Human apo
Ada61214	Human apo
Adj68447	Human hea
Adj83084	Human apo
Adj83086	Apolipop
Adj83087	Crab-eati
Adj83083	Human pro
Ade76862	Human pro
Adi119752	Human apo
Aap80668	Recombina
Abg97597	Human apo
Aao30162	Human apo
Aau33170	Novel hum
Abg97583	Human apo
Abg97584	Human apo
Abg97586	Human apo
Abg97585	Human apo
Abg97588	Human apo
Abg97589	Human apo
Abg97599	Human apo
Abg97596	Human apo
Abg97602	Human apo
Abg97601	Human apo
Abg97600	Human apo
Abg97603	Human apo
Abg97604	Human apo
Abg97605	Human apo
Abg97592	Human apo
Abg97594	Human apo
Abg97595	Human apo
Abg97606	Human apo
Aae24652	Human MSP
Aae24646	Human MSP
Aae24647	Human MSP
Aao02278	Human pol
Adj93927	Western E
Aau30268	Novel hum
Aao12095	Human pol
Abg63741	Drosophil
Abf30722	Rat angio
Adf30714	Rat angio
Adf30724	Rat angio
Adf30726	Rat angio
Ag21619	Arabidops
Ag21618	Arabidops
Ag21617	Arabidops
Ag08396	Arabidops
Ag08395	Arabidops

99	36	72.0	294	3	AAG08394	Rag08394 Arabidops	172	34	68.0	430	7	ADE96057	Ade96057 Human uri
100	36	72.0	428	6	AAU26010	Abu26010 Protein e	173	34	68.0	466	3	AAB43921	Aab43921 Human gas
101	35	70.0	47	4	AAO12396	Aao12396 Human pol	174	34	68.0	466	4	AAB63634	Aab63634 Human can
102	35	70.0	100	3	RAG00952	Rag00952 Human sec	175	34	68.0	475	7	ADC94239	Adc94239 E. faeciu
103	35	70.0	130	5	ADK35406	Adk35406 Novel hum	176	34	68.0	492	4	ABB52501	Abb52501 Escherich
104	35	70.0	137	4	AAU25867	Aau25867 Human pro	177	34	68.0	497	6	ABU47012	Abu47012 Protein e
105	35	70.0	138	6	ABP76299	Abp76299 Human GEN	178	34	68.0	507	7	ABR96048	Abr96048 Human uri
106	35	70.0	139	6	ABR69617	Abp69617 Human CGD	179	34	68.0	519	6	ABR40118	Abr40118 Human cel
107	35	70.0	139	6	ABR69656	Abp69656 Human CGD	180	34	68.0	550	4	AAW63674	Aaw63674 Polypepti
108	35	70.0	139	7	ABR69656	Abp69656 Human CGD	181	34	68.0	550	4	AAW63674	Aaw63674 Polypepti
109	35	70.0	139	7	ABR69656	Abp69656 Human CGD	182	34	68.0	550	4	AAW63674	Aaw63674 Polypepti
110	35	70.0	168	6	ABR69655	Abp69655 Human CGD	183	34	68.0	596	7	ADH86631	Adh86631 Enterococ
111	35	70.0	177	4	AAU81943	Aau81943 Human hae	184	34	68.0	607	7	ADH86631	Adh86631 Enterococ
112	35	70.0	188	5	ABP64799	Abp64799 Human pro	185	34	68.0	637	7	ADM05658	Adm05658 Human pro
113	35	70.0	188	5	ABR48482	Abp48482 Human Nat	186	34	68.0	663	7	ADH86631	Adh86631 Enterococ
114	35	70.0	188	7	ADG10828	Adg10828 Human STA	187	34	68.0	670	4	ABG12544	Abg12544 Novel hum
115	35	70.0	188	7	ADG10830	Adg10830 Human STA	188	34	68.0	821	4	ABG14530	Abg14530 Novel hum
116	35	70.0	188	8	ADG20487	Adg20487 Human NK4	189	34	68.0	821	4	ABG07875	Abg07875 Novel hum
117	35	70.0	194	4	AAU81880	Aau81880 Human hae	190	34	68.0	874	4	ABG10246	Abg10246 Novel hum
118	35	70.0	211	6	ADA52887	Ada52887 Human pro	191	34	68.0	932	7	ADH86631	Adh86631 Enterococ
119	35	70.0	211	6	ABU00128	Abu00128 Human nov	192	34	68.0	964	7	ADH86631	Adh86631 Enterococ
120	35	70.0	222	6	ABR58508	Abp58508 Human sec	193	34	68.0	967	6	ABR41060	Abr41060 Human MAP
121	35	70.0	234	6	ABR92129	Abp92129 Human cer	194	34	68.0	968	7	ADC31834	Adc31834 Human nov
122	35	70.0	234	6	ABR92128	Abp92128 Human cer	195	34	68.0	985	7	ADH86631	Adh86631 Enterococ
123	35	70.0	234	7	ADG10720	Adg10720 Human STA	196	34	68.0	985	7	ADH86631	Adh86631 Enterococ
124	35	70.0	234	7	ADG10832	Adg10832 Human STA	197	34	68.0	985	7	ADH86631	Adh86631 Enterococ
125	35	70.0	234	7	ADN95584	Adn95584 Human BEC	198	34	68.0	986	7	ADC31833	Adc31833 Human nov
126	35	70.0	234	8	ADJ75301	Adj75301 Marker ge	199	34	68.0	1009	7	ADH86631	Adh86631 Enterococ
127	35	70.0	245	7	ADJ68279	Adj68279 Human hea	200	34	68.0	1014	2	AAW63673	Aaw63673 Polypepti
128	35	70.0	245	7	ADJ68280	Adj68280 Human hea	201	34	68.0	1014	4	AAW63673	Aaw63673 Polypepti
129	35	70.0	259	3	RAG04623	Rag04623 Arabidops	202	34	68.0	1195	7	ADK64212	Adk64212 Disease t
130	35	70.0	287	3	RAG04622	Rag04622 Arabidops	203	34	68.0	1234	4	ABR68510	Abp68510 Drosophil
131	35	70.0	318	3	RAG04621	Rag04621 Arabidops	204	34	68.0	1588	8	ADH14288	Adh14288 Mouse ret
132	35	70.0	376	7	ADJ06455	Adj06455 Bacterial	205	34	68.0	1591	6	ABR41061	Abr41061 Human MAP
133	35	70.0	657	6	ABU48469	Abu48469 Protein e	206	34	68.0	1594	8	ADH14287	Adh14287 Human ret
134	35	70.0	1102	4	ABG29358	Abg29358 Novel hum	207	34	68.0	1644	4	ABG12176	Abg12176 Novel hum
135	35	70.0	1102	8	ADJ57489	Adj57489 Human pol	208	34	68.0	2033	8	ADJ75622	Adj75622 Marker ge
136	35	70.0	1342	8	ADJ57463	Adj57463 Breast ca	209	34	68.0	2033	8	ADJ75622	Adj75622 Marker ge
137	35	70.0	1456	8	ABG29357	Abg29357 Novel hum	210	33	66.0	45	8	ABO56509	Abp56509 Human gen
138	35	70.0	1456	8	ADJ57490	Adj57490 Human pol	211	33	66.0	114	2	AAW76562	Aaw76562 Human ova
139	34	68.0	67	5	ABP04319	Abp04319 Human ORF	212	33	66.0	138	4	AAW42205	Aaw42205 Human pol
140	34	68.0	78	4	AAU22150	Aau22150 Human car	213	33	66.0	148	2	AAW28082	Aaw28082 Staphyloc
141	34	68.0	78	7	ADK64118	Adk64118 Human car	214	33	66.0	159	4	AAU33520	Aau33520 Enterococ
142	34	68.0	80	4	AAU22036	Aau22036 Human dig	215	33	66.0	194	2	AAU33552	Aau33552 Staphyloc
143	34	68.0	80	4	AAU22036	Aau22036 Human liv	216	33	66.0	194	2	AAW85110	Aaw85110 Thyroid h
144	34	68.0	80	5	ABP40897	Abp40897 Human liv	217	33	66.0	194	2	AAW92398	Aaw92398 Human TR-
145	34	68.0	80	7	ADJ15015	Adj15015 Human liv	218	33	66.0	194	2	AAW40591	Aaw40591 Partial a
146	34	68.0	96	4	AAU92666	Aau92666 Human dig	219	33	66.0	228	6	ABU43725	Abu43725 Staphyloc
147	34	68.0	96	4	AAU22660	Aau22660 Novel hum	220	33	66.0	230	6	ABU43725	Abu43725 Protein e
148	34	68.0	96	7	ADH32500	Adh32500 Human nov	221	33	66.0	230	6	ABU43725	Abu43725 Protein e
149	34	68.0	113	5	ABG93329	Abg93329 C. albica	222	33	66.0	231	6	ABU16228	Abu16228 Staphyloc
150	34	68.0	123	5	ABP08632	Abp08632 Human ORF	223	33	66.0	231	6	ABU16228	Abu16228 Staphyloc
151	34	68.0	143	4	ADM20065	Adm20065 Protein e	224	33	66.0	231	6	ABM71195	Abm71195 Staphyloc
152	34	68.0	175	6	ABU29509	Abu29509 Protein e	225	33	66.0	233	5	ABU49740	Abu49740 Listeria
153	34	68.0	179	4	AAO00017	Aao00017 Human pol	226	33	66.0	233	5	ABU49740	Abu49740 Listeria
154	34	68.0	197	7	ADC94507	Adc94507 E. faeciu	227	33	66.0	235	5	ABP40300	Abp40300 Staphyloc
155	34	68.0	225	7	ABM73793	Abm73793 DNA clone	228	33	66.0	239	6	ABU29773	Abu29773 Protein e
156	34	68.0	234	4	ABG14913	Abg14913 Novel hum	229	33	66.0	240	4	AAU38766	Aau38766 Human pol
157	34	68.0	237	4	ABR63635	Abp63635 Human gas	230	33	66.0	240	5	ABM75727	Abm75727 Human RNA
158	34	68.0	271	6	ABR53465	Abp53465 Protein s	231	33	66.0	240	5	ABU25456	Abu25456 Protein e
159	34	68.0	271	7	ADK64594	Adk64594 Disease t	232	33	66.0	241	3	AAU41492	Aau41492 Arabidops
160	34	68.0	275	7	ADH86631	Adh86631 Enterococ	233	33	66.0	244	3	AAU41491	Aau41491 Arabidops
161	34	68.0	336	7	ADH86631	Adh86631 Enterococ	234	33	66.0	244	3	AAU41491	Aau41491 Arabidops
162	34	68.0	422	3	AAU52399	Aau52399 Human ker	235	33	66.0	249	7	ADC90306	Adc90306 Novel hum
163	34	68.0	422	3	AAU52399	Aau52399 Human ker	236	33	66.0	249	7	ADC90306	Adc90306 Novel hum
164	34	68.0	422	5	ABG96336	Abg96336 Human ova	237	33	66.0	257	4	AAU35088	Aau35088 Enterococ
165	34	68.0	422	5	AAE20424	Aae20424 Human ker	238	33	66.0	262	4	AAU35088	Aau35088 Enterococ
166	34	68.0	422	5	ABP54685	Abp54685 Metastati	239	33	66.0	262	4	AAU35088	Aau35088 Enterococ
167	34	68.0	422	7	ABM78946	Abm78946 Breast ca	240	33	66.0	298	7	ADH86631	Adh86631 Enterococ
168	34	68.0	422	8	ADJ75461	Adj75461 Marker ge	241	33	66.0	299	4	AAU35088	Aau35088 Enterococ
169	34	68.0	422	8	ADJ76249	Adj76249 Marker ge	242	33	66.0	323	3	AAU41490	Aau41490 Arabidops
170	34	68.0	422	8	ADJ75484	Adj75484 Marker ge	243	33	66.0	365	4	AAU93464	Aau93464 Human pol
171	34	68.0	422	8	ADJ76236	Adj76236 Marker ge	244	33	66.0	365	4	AAU40421	Aau40421 Human pol

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OM protein - protein search, using sw model

Run on: January 28, 2005, 18:55:58 ; Search time 40 Seconds
(without alignments)
24.054 Million cell updates/sec

Title: US-09-991-627-2
Perfect score: 50
Sequence: 1 NLEKETEGLR 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	241	2 A24998	apolipoprotein A-I
2	50	100.0	265	1 LPRB1B	apolipoprotein A-I
3	50	100.0	266	1 LPRB1Z	apolipoprotein A-I
4	50	100.0	267	1 A26529	apolipoprotein A-I
5	50	100.0	267	1 LPHUA1	apolipoprotein A-I
6	50	100.0	267	2 JS0079	apolipoprotein A-I
7	44	88.0	231	2 JQ0704	apolipoprotein A-I
8	44	88.0	264	2 S11394	apolipoprotein A-I
9	44	88.0	265	2 A46018	apolipoprotein A-I
10	41	82.0	266	1 LPDGA1	apolipoprotein A-I
11	39	78.0	199	2 T08465	ubiquitin-protein
12	39	78.0	259	2 A24700	apolipoprotein A-I
13	39	78.0	389	2 A40809	enamelin, 44K - bo
14	38	76.0	265	2 J70672	apolipoprotein A-I
15	38	76.0	265	2 A56858	apolipoprotein A-I
16	37	74.0	978	2 A70387	conserved hypother
17	36	72.0	262	2 JCL137	apolipoprotein A-I
18	36	72.0	264	2 S22420	apolipoprotein A-I
19	36	72.0	282	2 F86396	hypothetical prote
20	36	72.0	294	2 H96719	homeobox gene 13 p
21	36	72.0	301	2 T14331	homeotic protein -
22	35	70.0	117	2 S28124	gas-vesicle operon
23	35	70.0	137	2 H69110	hypothetical prote
24	35	70.0	234	2 I56140	NK and T lymphocyt
25	35	70.0	318	2 T49167	hypothetical prote
26	35	70.0	448	2 T23263	hypothetical prote
27	35	70.0	621	2 A32838	DNA-directed RNA p
28	35	70.0	625	2 B42361	DNA-directed RNA p
29	35	70.0	625	2 AE2005	RNA polymerase gam

30	70.0	657	2 B71367	probable rep helic
31	70.0	1606	2 T34073	paramerin - chicke
32	70.0	1840	2 T29091	transitin - chicke
33	68.0	114	2 D84984	hypothetical prote
34	68.0	142	2 I48282	gene CCl1 protein -
35	68.0	188	2 T44948	flagella-related p
36	68.0	222	2 AE0276	dethiobiotin synth
37	68.0	254	2 F70347	molybdenum cofacto
38	68.0	573	2 A86253	hypothetical prote
39	68.0	1014	2 JE0333	klotho protein - r
40	68.0	1195	2 S38174	probable purine nu
41	68.0	1290	2 A55094	chromosomal protei
42	68.0	2823	2 F87908	protein T22A3.8 [i
43	68.0	2823	2 T23064	hypothetical prote
44	68.0	3102	2 T43291	laminin alpha chai
45	66.0	156	2 B87641	transcription regu
46	66.0	213	2 F71696	hypothetical prote
47	66.0	231	2 E89960	hypothetical prote
48	66.0	233	2 AF1367	16S pseudouridyat
49	66.0	233	2 AG1736	16S pseudouridyat
50	66.0	250	2 F83474	hypothetical prote
51	66.0	397	2 C72354	conserved hypother
52	66.0	405	2 AF2735	DNA-damage inducib
53	66.0	407	2 A97149	molybdopterin bios
54	66.0	424	2 JC5891	omega 6 desaturase
55	66.0	434	2 T32520	hypothetical prote
56	66.0	437	2 F97516	DNA damage inducib
57	66.0	438	2 T33601	hypothetical prote
58	66.0	464	2 E83834	flagellin B1477 [
59	66.0	509	2 A43580	coccolysin [EC 3.4
60	66.0	939	2 T32521	hypothetical prote
61	66.0	1381	1 S45781	probable calcium-b
62	66.0	1474	2 T18281	hypothetical prote
63	64.0	133	2 JE0311	serine proteinase
64	64.0	144	1 TVPBD	small T antigen -
65	64.0	211	1 ZKBF74	transcription regu
66	64.0	248	2 T33230	hypothetical prote
67	64.0	263	2 E86215	protein T6D22.16 [
68	64.0	309	2 B96602	hypothetical prote
69	64.0	320	2 G84676	hypothetical prote
70	64.0	320	2 T32519	hypothetical prote
71	64.0	372	2 T24891	hypothetical prote
72	64.0	379	2 AD1974	thiamin-phosphate
73	64.0	380	2 A42832	factor VIII-associ
74	64.0	384	2 T24075	hypothetical prote
75	64.0	396	1 XNECD	aspartate transami
76	64.0	396	2 AD0616	aspartate aminotra
77	64.0	396	2 A85619	aspartate aminotra
78	64.0	396	2 C90755	aspartate aminotra
79	64.0	413	2 T43810	methylaspartate am
80	64.0	413	2 A85575	probable methylasp
81	64.0	413	2 A99724	3-methylaspartate
82	64.0	434	2 C82516	type I restriction
83	64.0	430	2 A87708	hypothetical prote
84	64.0	438	2 T52082	alpha galactosyltr
85	64.0	475	1 WMDP6	early E1B 53K prot
86	64.0	489	1 S66088	conserved hypother
87	64.0	554	1 TVPBP	large T antigen -
88	64.0	575	2 C83113	probable type II s
89	64.0	596	2 T17333	hypothetical prote
90	64.0	607	2 H90590	hypothetical prote
91	64.0	609	2 S55270	catrocollastatin p
92	64.0	678	2 S44925	IB3/5-polypeptide
93	64.0	792	2 F83304	probable restricti
94	64.0	793	2 E64545	hypothetical prote
95	64.0	817	2 T03852	protein phosphatas
96	64.0	873	2 T05189	guananyl aminopept
97	64.0	902	2 S33918	dynam-like prote
98	64.0	916	2 F71962	hypothetical prote
99	64.0	932	2 S65214	probable alpha/gam
100	64.0	976	2 D96714	DNA-directed RNA p
101	64.0	980	2 E86589	CR590 hypother
102	64.0	980	2 E72035	conserved hypother

103	32	64.0	992	2	T46337	hypothetical prote	176	31	62.0	649	2	C32575	C-ski protein FB27
104	32	64.0	1073	2	S69079	hypothetical prote	177	31	62.0	654	2	T33044	hypothetical prote
105	32	64.0	1277	2	T15109	hypothetical prote	178	31	62.0	684	1	TVHUSN	transforming prote
106	32	64.0	1396	2	F87311	DNA-directed RNA p	179	31	62.0	690	2	I51298	transforming prote
107	32	64.0	1532	2	H96795	hypothetical prote	180	31	62.0	713	2	B32575	C-ski protein FB28
108	32	64.0	2254	2	D86215	protein T6D22.14 [181	31	62.0	717	1	S29923	transforming prote
109	32	64.0	2677	2	T31394	desmoplakin I - hu	182	31	62.0	727	1	A38206	procollagen-lysine
110	32	64.0	4151	2	T13734	groovin gene prote	183	31	62.0	728	1	TVHUSK	transforming prote
111	31	62.0	99	2	B46598	ski-related protei	184	31	62.0	728	2	S59964	procollagen-lysine
112	31	62.0	101	2	A46598	transforming prote	185	31	62.0	750	2	A32575	C-ski protein FB29
113	31	62.0	116	2	H90133	40S ribosomal prot	186	31	62.0	924	2	S06117	myosin heavy chain
114	31	62.0	125	2	T05633	hypothetical prote	187	31	62.0	930	2	T34334	hypothetical prote
115	31	62.0	141	2	F64411	hypothetical prote	188	31	62.0	961	2	AD0548	puative autotransp
116	31	62.0	157	2	T24917	hypothetical prote	189	31	62.0	971	2	A35697	transcription fact
117	31	62.0	181	1	Z4BPT9	ribonucleoside-tri	190	31	62.0	980	2	H90581	probable flagellin
118	31	62.0	190	2	T23702	hypothetical prote	191	31	62.0	980	2	D85532	probable structura
119	31	62.0	209	2	S32681	DNA-directed RNA p	192	31	62.0	1005	2	A64465	hypothetical prote
120	31	62.0	223	2	AB1541	ABC transporters,	193	31	62.0	1053	2	T09645	DNA-directed RNA p
121	31	62.0	224	2	AD1407	ribulose-5-phospha	194	31	62.0	1191	2	B97116	chromosome segrega
122	31	62.0	224	2	AD1783	probable pseudouri	195	31	62.0	1206	2	T44376	DNA-directed RNA p
123	31	62.0	235	2	H72025	pseudouridine synt	196	31	62.0	1218	2	T29315	hypothetical prote
124	31	62.0	235	2	F86598	ribosomal large ch	197	31	62.0	1227	2	B96673	hypothetical prote
125	31	62.0	235	2	G81515	ribosomal large ch	198	31	62.0	1251	2	H86194	hypothetical prote
126	31	62.0	238	2	B72320	ribonuclease Hf1 -	199	31	62.0	1265	2	T07397	hypothetical prote
127	31	62.0	241	2	B81741	ribosomal large ch	200	31	62.0	1410	1	A57013	early endosome ant
128	31	62.0	241	2	F71478	probable pseudouri	201	31	62.0	1478	2	S78131	DNA-directed RNA p
129	31	62.0	261	2	T16732	hypothetical prote	202	31	62.0	1507	2	T42631	breast cancer tumo
130	31	62.0	273	2	H86904	hypothetical prote	203	31	62.0	1837	2	T41023	probable nuclear p
131	31	62.0	286	1	D64775	acyl-CoA thioleste	204	31	62.0	1976	2	A59252	myosin heavy chain
132	31	62.0	286	2	A37053	flagellar filament	205	31	62.0	2007	1	B43402	myosin heavy chain
133	31	62.0	286	2	AD0560	acyl-CoA thioester	206	31	62.0	2606	2	T03159	large tegument pro
134	31	62.0	286	2	F85542	acyl-CoA thioester	207	30	60.0	90	2	C64013	hypothetical prote
135	31	62.0	286	2	B90692	acyl-CoA thioester	208	30	60.0	100	2	B87184	conserved hypothet
136	31	62.0	286	2	S07533	puff II/9A-2 prote	209	30	60.0	132	2	A96600	protein F14J16.12
137	31	62.0	287	2	A27082	2,4-dichlorophenox	210	30	60.0	134	2	A44173	calcitonin gene-re
138	31	62.0	288	1	S42566	protein kinase (EC	211	30	60.0	142	2	A87653	CheE protein limpo
139	31	62.0	300	2	A81418	pseudouridyate sy	212	30	60.0	145	2	S62510	hypothetical prote
140	31	62.0	303	2	F71680	hypothetical prote	213	30	60.0	146	2	H69446	hypothetical prote
141	31	62.0	304	1	FLB568	flagellin (hag) -	214	30	60.0	166	2	T39586	rna binding protei
142	31	62.0	304	2	D72316	ribosomal large su	215	30	60.0	174	2	T28844	hypothetical prote
143	31	62.0	305	2	T09370	shikimate kinase h	216	30	60.0	196	2	D84178	SOS ribosomal prot
144	31	62.0	321	2	G64463	hypothetical prote	217	30	60.0	203	2	T32346	hypothetical prote
145	31	62.0	350	2	C97276	mannose-1-phospat	218	30	60.0	206	1	E64327	H+-transporting tw
146	31	62.0	353	2	F84252	phycocyanin alpha	219	30	60.0	208	2	AB1706	hypothetical prote
147	31	62.0	354	2	C90173	3-dehydroquinatase	220	30	60.0	212	1	A49436	dual specificity p
148	31	62.0	374	2	D81937	probable ribosomal	221	30	60.0	219	2	I52911	cytoskeletal prote
149	31	62.0	374	2	AB1168	ribosomal large ch	222	30	60.0	219	2	C91117	probable 2-compone
150	31	62.0	388	2	S26964	flavohemoglobin -	223	30	60.0	219	2	T02114	hypothetical prote
151	31	62.0	399	1	A26916	ribonucleoside-dip	224	30	60.0	231	2	S73469	probable lipoprote
152	31	62.0	429	2	AC1163	flagellar hook-ass	225	30	60.0	233	2	H86593	Yop translocation
153	31	62.0	429	2	AC1522	flagellar hook-ass	226	30	60.0	233	2	D72030	type III secretion
154	31	62.0	442	2	T34661	hypothetical prote	227	30	60.0	241	2	I51211	cytoskeletal prote
155	31	62.0	465	2	T08290	hypothetical prote	228	30	60.0	241	2	S49014	lysine - lactococcu
156	31	62.0	466	2	AB1126	endo-1,4-beta-xyla	229	30	60.0	250	2	T13459	hypothetical prote
157	31	62.0	467	2	F64765	yaiU protein - Esc	230	30	60.0	257	2	AB1208	extragenic suppres
158	31	62.0	475	2	A34443	nitrogen fixation	231	30	60.0	257	2	AE1564	extragenic suppres
159	31	62.0	475	2	AG1995	nitrogen fixation	232	30	60.0	263	1	AB0209	iclr-family transc
160	31	62.0	491	2	F87793	protein C2A12.6 [233	30	60.0	265	1	E69864	myo-inositol-1(or
161	31	62.0	521	1	VG1VDH	envelope glycoprot	234	30	60.0	285	1	B69025	conserved hypothet
162	31	62.0	544	2	S25101	CTP synthase (EC 6	235	30	60.0	278	1	B69025	translation elonga
163	31	62.0	572	2	T32523	hypothetical prote	236	30	60.0	281	2	T34810	hypothetical prote
164	31	62.0	579	2	B86565	oligopeptide perme	237	30	60.0	289	2	T48894	lipoprotein mtaA,
165	31	62.0	579	2	C72059	peptide ABC transp	238	30	60.0	290	2	T40031	hypothetical prote
166	31	62.0	596	2	D84972	ABC transporter At	239	30	60.0	290	2	G97328	uncharacterized co
167	31	62.0	599	2	A48663	limonene cyclase -	240	30	60.0	292	1	C64503	conserved hypothet
168	31	62.0	601	2	A53318	malate dehydrogena	241	30	60.0	301	1	S19209	protein kinase (EC
169	31	62.0	608	2	E71859	phosphogluconate d	242	30	60.0	303	2	A87616	hydrolase, carbon-
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171	31	62.0	619	2	B86617	CT858 hypothetical	244	30	60.0	310	2	T11551	adhesin - Streptoc
172	31	62.0	619	2	F72006	CT858 hypothetical	245	30	60.0	314	2	T23178	hypothetical prote
173	31	62.0	623	2	A49112	sodium-glucose cot	246	30	60.0	318	2	C71168	hypothetical prote
174	31	62.0	632	2	T38617	probable ubiquitin	247	30	60.0	326	2	S50713	probable phosphoe
175	31	62.0	646	2	T33346	hypothetical prote	248	30	60.0	330	2	JC5935	exostose-related p

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OM protein - protein search, using sw model

Run on: January 28, 2005, 18:56:43 ; Search time 38 Seconds
(without alignments)
17.452 Million cell updates/sec

Title: US-09-991-627-2

Perfect score: 50

Sequence: 1 NLEKETEGRLR 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	200	3	US-08-952-796-15
2	50	100.0	243	4	US-09-079-030-119
3	50	100.0	264	1	US-08-448-606-6
4	50	100.0	267	1	US-07-959-946-3
5	50	100.0	267	1	US-08-333-577-3
6	50	100.0	267	3	US-08-952-796-2
7	50	100.0	267	4	US-08-940-136-260
8	50	100.0	267	4	US-09-919-039-27
9	50	100.0	267	5	PCT-US92-08634-3
10	35	70.0	100	4	US-09-513-999C-5033
11	35	70.0	188	4	US-10-000-489-60
12	35	70.0	376	4	US-09-543-681A-6740
13	34	68.0	137	4	US-09-248-796A-14477
14	34	68.0	197	4	US-09-07-532A-1134
15	34	68.0	422	2	US-09-067-351-3
16	34	68.0	422	3	US-09-360-490-3
17	34	68.0	470	4	US-09-886-319A-35
18	34	68.0	475	4	US-09-107-532A-3866
19	34	68.0	550	4	US-09-344-510B-4
20	34	68.0	596	4	US-09-134-000C-4516
21	34	68.0	1014	4	US-09-344-510B-3
22	34	68.0	1195	4	US-09-538-092-517
23	33	66.0	235	3	US-09-134-001C-5145
24	33	66.0	249	4	US-09-107-532A-4520
25	33	66.0	432	4	US-09-917-254-80
26	33	66.0	519	4	US-09-134-000C-4482
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28	32	64.0	54	2	US-08-293-284A-13
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78	31	62.0	1263	4	US-09-677-488A-11
79	31	62.0	1263	4	US-09-677-682B-11
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87	30	60.0	137	4	US-09-134-000C-5507
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97	30	60.0	152	4	US-08-311-731A-272
98	30	60.0	153	4	US-09-270-767-35615
99	30	60.0	153	4	US-09-270-767-50832
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101	30	60.0	189	4	US-09-270-767-37522	Sequence 37522, A	174	29	58.0	141	3	US-08-944-604-14	Sequence 14, Appl
102	30	60.0	189	4	US-09-270-767-52739	Sequence 52739, A	175	29	58.0	160	4	US-09-489-039A-13473	Sequence 13473, A
103	30	60.0	212	1	US-08-461-859-35	Sequence 35, Appl	176	29	58.0	162	4	US-09-489-039A-7850	Sequence 7850, Ap
104	30	60.0	212	4	US-09-917-254-62	Sequence 62, Appl	177	29	58.0	170	3	US-08-858-207A-519	Sequence 519, App
105	30	60.0	216	4	US-09-198-452A-627	Sequence 627, App	178	29	58.0	171	4	US-09-248-796A-18229	Sequence 18229, A
106	30	60.0	219	3	US-08-952-127-19	Sequence 19, Appl	179	29	58.0	175	4	US-09-252-991A-20191	Sequence 20191, A
107	30	60.0	254	4	US-09-270-767-64583	Sequence 44283, A	180	29	58.0	208	4	US-09-107-532A-6124	Sequence 6124, Ap
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109	30	60.0	336	4	US-09-673-395A-600	Sequence 600, App	182	29	58.0	226	4	US-09-248-796A-14924	Sequence 14924, A
110	30	60.0	341	4	US-09-538-092-305	Sequence 305, App	183	29	58.0	228	4	US-09-252-991A-18371	Sequence 18371, A
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112	30	60.0	355	4	US-09-248-796A-18246	Sequence 18246, A	185	29	58.0	242	3	US-08-977-865-4	Sequence 4, Appli
113	30	60.0	374	4	US-09-252-991A-27773	Sequence 27773, A	186	29	58.0	259	4	US-09-540-236-2575	Sequence 2575, Ap
114	30	60.0	382	2	US-08-477-451-28	Sequence 28, Appl	187	29	58.0	263	4	US-09-583-110-3014	Sequence 3014, Ap
115	30	60.0	396	4	US-09-800-729-207	Sequence 207, App	188	29	58.0	289	3	US-08-961-083-20	Sequence 20, Appl
116	30	60.0	397	4	US-09-079-030-123	Sequence 123, App	189	29	58.0	289	4	US-09-536-784-20	Sequence 20, Appl
117	30	60.0	432	4	US-09-792-024-104	Sequence 104, App	190	29	58.0	291	3	US-09-443-184-54	Sequence 54, Appl
118	30	60.0	447	4	US-09-248-796A-14846	Sequence 14846, A	191	29	58.0	293	4	US-09-071-035-496	Sequence 496, App
119	30	60.0	453	4	US-09-583-110-4631	Sequence 4631, Ap	192	29	58.0	294	4	US-09-103-664A-5	Sequence 5, Appli
120	30	60.0	481	4	US-09-252-991A-31018	Sequence 31018, A	193	29	58.0	309	2	US-08-715-131-2	Sequence 2, Appli
121	30	60.0	519	3	US-08-997-445D-2	Sequence 2, Appli	194	29	58.0	309	3	US-09-221-753-2	Sequence 2, Appli
122	30	60.0	650	1	US-08-224-657-97	Sequence 97, Appl	195	29	58.0	309	4	US-09-583-110-3218	Sequence 3218, Ap
123	30	60.0	650	3	US-09-354-138-97	Sequence 97, Appl	196	29	58.0	309	4	US-09-754-809-2	Sequence 2, Appli
124	30	60.0	662	1	US-08-224-657-94	Sequence 94, Appl	197	29	58.0	313	4	US-09-543-681A-5250	Sequence 2520, Ap
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127	30	60.0	785	4	US-09-134-000C-6690	Sequence 6690, Ap	200	29	58.0	317	4	US-09-583-110-4111	Sequence 4111, Ap
128	30	60.0	816	4	US-10-101-464A-827	Sequence 827, App	201	29	58.0	318	4	US-08-555-755C-6	Sequence 6, Appli
129	30	60.0	867	2	US-08-938-365-2	Sequence 2, Appli	202	29	58.0	333	4	US-09-107-532A-4544	Sequence 4544, Ap
130	30	60.0	954	2	US-08-749-169A-3	Sequence 3, Appli	203	29	58.0	347	4	US-09-543-681A-5961	Sequence 5961, Ap
131	30	60.0	954	2	US-09-130-032A-3	Sequence 3, Appli	204	29	58.0	368	2	US-08-869-137-2	Sequence 2, Appli
132	30	60.0	954	4	US-09-866-028-7	Sequence 7, Appli	205	29	58.0	370	4	US-09-270-767-46593	Sequence 46593, A
133	30	60.0	954	4	US-09-944-457-7	Sequence 7, Appli	206	29	58.0	383	1	US-08-464-523B-31	Sequence 31, Appl
134	30	60.0	955	4	US-09-798-051-8	Sequence 8, Appli	207	29	58.0	390	4	US-08-977-865-2	Sequence 2, Appli
135	30	60.0	1068	3	US-09-085-199B-11	Sequence 11, Appl	208	29	58.0	401	4	US-09-491-577-56	Sequence 56, Appl
136	30	60.0	1240	4	US-10-101-464A-976	Sequence 976, App	209	29	58.0	407	2	US-08-334-846-4	Sequence 4, Appli
137	30	60.0	1288	4	US-09-919-039-209	Sequence 209, App	210	29	58.0	407	3	US-09-238-557-4	Sequence 4, Appli
138	30	60.0	1781	2	US-08-477-451-11	Sequence 11, Appl	211	29	58.0	414	4	US-08-836-687B-32	Sequence 32, Appl
139	30	60.0	1972	4	US-08-875-435B-3	Sequence 3, Appli	212	29	58.0	418	2	US-08-934-846-2	Sequence 2, Appli
140	30	60.0	3056	1	US-08-508-836A-8	Sequence 8, Appli	213	29	58.0	418	3	US-09-238-557-2	Sequence 2, Appli
141	30	60.0	3056	2	US-08-629-001A-3	Sequence 3, Appli	214	29	58.0	442	3	US-09-032-365A-17	Sequence 17, Appl
142	30	60.0	3056	2	US-08-874-266-2	Sequence 2, Appli	215	29	58.0	454	4	US-09-198-452A-197	Sequence 197, App
143	30	60.0	3056	3	US-08-642-274D-3	Sequence 3, Appli	216	29	58.0	491	3	US-08-812-824-1	Sequence 1, Appli
144	30	60.0	3056	3	US-08-952-127-3	Sequence 3, Appli	217	29	58.0	502	4	US-09-540-236-3780	Sequence 3780, Ap
145	30	60.0	3056	3	US-08-952-127-3	Sequence 3, Appli	218	29	58.0	516	4	US-09-107-532A-7034	Sequence 7034, Ap
146	30	60.0	3056	4	US-09-360-416-2	Sequence 2, Appli	219	29	58.0	534	4	US-09-103-664A-2	Sequence 2, Appli
147	30	60.0	3056	4	US-08-984-090-2	Sequence 2, Appli	220	29	58.0	568	3	US-09-134-001C-3768	Sequence 3768, Ap
148	30	60.0	3057	4	US-09-360-416-3	Sequence 3, Appli	221	29	58.0	590	4	US-09-248-796A-14494	Sequence 14494, A
149	30	60.0	3666	2	US-08-222-617A-12	Sequence 12, Appl	222	29	58.0	593	1	US-07-561-522-4	Sequence 4, Appli
150	30	60.0	3727	2	US-08-222-617A-27	Sequence 27, Appl	223	29	58.0	593	1	US-08-217-438-4	Sequence 4, Appli
151	30	60.0	3778	2	US-08-222-617A-2	Sequence 2, Appli	224	29	58.0	593	1	US-08-487-890A-100	Sequence 100, App
152	29	58.0	35	2	US-08-491-527A-1	Sequence 1, Appli	225	29	58.0	593	1	US-08-321-978-4	Sequence 4, Appli
153	29	58.0	35	2	US-08-845-659-1	Sequence 1, Appli	226	29	58.0	593	2	US-08-710-584-4	Sequence 4, Appli
154	29	58.0	35	3	US-08-845-658-1	Sequence 1, Appli	227	29	58.0	593	2	US-08-478-435-100	Sequence 100, App
155	29	58.0	35	3	US-09-518-178-1	Sequence 1, Appli	228	29	58.0	593	2	US-08-337-483-100	Sequence 100, App
156	29	58.0	35	4	US-09-517-597-1	Sequence 1, Appli	229	29	58.0	593	2	US-08-478-373-100	Sequence 100, App
157	29	58.0	57	3	US-09-015-030-11	Sequence 11, Appl	230	29	58.0	593	2	US-08-474-671-100	Sequence 100, App
158	29	58.0	62	4	US-09-513-990C-7101	Sequence 7101, Ap	231	29	58.0	593	3	US-08-483-577A-100	Sequence 100, App
159	29	58.0	74	3	US-09-134-001C-5666	Sequence 5666, Ap	232	29	58.0	593	3	US-08-897-438-100	Sequence 100, App
160	29	58.0	80	4	US-09-513-990C-6128	Sequence 6128, Ap	233	29	58.0	593	3	US-08-637-654-100	Sequence 100, App
161	29	58.0	89	4	US-09-134-000C-6216	Sequence 6216, Ap	234	29	58.0	593	3	US-08-649-518-100	Sequence 100, App
162	29	58.0	92	4	US-09-248-796A-24089	Sequence 24089, A	235	29	58.0	593	3	US-08-753-750B-14	Sequence 14, Appl
163	29	58.0	114	4	US-09-513-990C-5016	Sequence 5016, Ap	236	29	58.0	620	4	US-09-538-092-1285	Sequence 1285, Ap
164	29	58.0	121	2	US-08-658-639-13	Sequence 13, Appl	237	29	58.0	637	4	US-09-817-310-2	Sequence 2, Appli
165	29	58.0	121	3	US-08-944-604-13	Sequence 13, Appl	238	29	58.0	662	3	US-09-061-768A-25	Sequence 25, Appl
166	29	58.0	121	4	US-09-248-796A-22471	Sequence 22471, A	239	29	58.0	662	4	US-09-764-246-25	Sequence 25, Appl
167	29	58.0	121	4	US-09-248-796A-26597	Sequence 26597, A	240	29	58.0	712	1	US-08-121-713D-64	Sequence 64, Appl
168	29	58.0	126	4	US-09-107-532A-4794	Sequence 4794, Ap	241	29	58.0	712	1	US-08-835-268-64	Sequence 64, Appl
169	29	58.0	129	4	US-09-134-000C-6748	Sequence 6748, Ap	242	29	58.0	712	2	US-09-060-692-64	Sequence 64, Appl
170	29	58.0	129	4	US-09-583-110-4161	Sequence 4161, Ap	243	29	58.0	712	3	US-08-833-391-64	Sequence 64, Appl
171	29	58.0	134	4	US-09-270-767-31690	Sequence 31690, A	244	29	58.0	712	3	US-09-060-610-64	Sequence 64, Appl
172	29	58.0	134	4	US-09-270-767-46907	Sequence 46907, A	245	29	58.0	712	5	PCT-US94-10151A-64	Sequence 64, Appl
173	29	58.0	141	2	US-08-658-639-14	Sequence 14, Appl	246	29	58.0	712			